

WHAT IS CLAIMED IS:

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1. A nucleic acid comprising at least 50 contiguous bases from an *rpoB* sequence shown in Table 1.

2. The nucleic acid of claim 1 comprising a complete rpoB sequence shown in Table 1.

3. A set of probes perfectly complementary to and spanning a full-length sequence shown in Table 1.

4. A method of classifying a mycobacteria, comprising

- providing a sample comprising a mycobacterial rpoB target nucleic acid from a mycobacteria;
- determining the sequence of a segment of at least 50 contiguous bases from the target nucleic acid;
- comparing the determined sequence to at least one sequence shown in Table 1;
- classifying the mycobacteria from the extent of similarity of the compared sequences.

5. The method of claim 4, wherein at least 100 contiguous bases are determined from the target nucleic acid.

6. The method of claim 4, wherein the determined sequence is compared with at least ten sequences shown in Table 1.

7. A method of classifying a mycobacteria, comprising

providing a sample comprising a mycobacterial rpoB target nucleic acid;

determining the identity of one or more bases in the target sequence at one or more positions corresponding to one or more of the highlighted positions in a sequence shown in

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8 Table 1, the identity of the one or more bases characterizing
9 the species of mycobacteria that is present in the sample.

1 8. The method of claim 7, wherein the identity of
2 at least 10 bases in the target nucleic acid at positions
3 corresponding to highlighted positions in a sequence shown in
4 Table 1 is determined.

1 9. The method of claim 8, wherein the identity of
2 at least 20 bases in the target sequence at highlighted
3 positions shown in Table 1 are identified.

1 10. The method of claim 9, further comprising
2 comparing the 20 determined bases with 20 bases occupying
3 corresponding positions in each of at least ten sequences from
4 Table 1.

1 11. A sequence-specific polynucleotide probe or
2 primer that hybridizes to a segment of a mycobacterial rpoB
3 sequence shown in Table 1 or its complement without
4 hybridizing to the M. tuberculosis sequence designated ATCC9-
5 Mtb in Table 1 or its complement, wherein the segment includes
6 a highlighted nucleotide position shown in Table 1.

1 12. The sequence-specific polynucleotide of claim 9
2 that is a probe.

1 13. The sequence-specific polynucleotide of
2 claim 10, wherein a central position of the probe aligns with
3 a highlighted nucleotide position shown in Tables 13.

1 14. The sequence-specific polynucleotide of claim 9
2 that is a primer.

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